

What is claimed is:

1. A recombinant polynucleotide selected from the group consisting of:

(a) a nucleotide sequence encoding a polypeptide, wherein said nucleotide sequence is selected from

the group consisting of SEQ ID NO: 2N - 1, where N = 1- 335, SEQ ID NOs: 671, 672, 673, 674, 675, 676, 677, 678, 679, 680, 684, 685, 686, 687, 688, 689, 691, 692, 693, 694, 695, 696, 697, 698, 699, 701, 702, 704, 705, 706, 708, 709, 710, 711, 712, 713, 714, 716, 717, 718, 719, 720, 721, 722, 723, 724, 725, 726, 727, 728, 732, 733, 734, 735, 736, 737, 738, 739, 740, 741, 742, 744, 745, 746, 747, 748, 749, 750, 751, 752, 753, 754, 755, 756, 757, 758, 759, 764, 765, 768, 769, 770, 771, 772, 773, 774, 775, 776, 777, 778, 779, 780, 781, 786, 787, 788, 789, 790, 791, 792, 793, 794, 795, 796, 797, 798, 799, 800, 801, 802, 803, 804, 805, 806, 812, 813, 814, 815, 816, 817, 818, 819, 820, 821, 822, 823, 824, 825, 826, 827, 828, 829, 834, 835, 836, 837, 838, 839, 840, 841, 842, 843, 844, 853, 854, 855, 856, 857, 858, 859, 860, 861, 862, 863, 864, 866, 867, 868, 869, 870, 871, 874, 875, 876, 877, 878, 879, 880, 881, 882, 883, 884, 888, 889, 890, 891, 892, 893, 894, 895, 896, 897, 899, 900, 901, 902, 903, 904, 905, 906, 907, 909, 910, 911, 912, 913, 914, 915, 916, 917, 918, 920, 921, 922, 923, 924, 926, 927, 928, 929, 930, 931, 938, 939, 940, 941, 942, 944, 945, 946, 947, 948, 949, 950, 951, 952, 953, 954, 955, 960, 961, 962, 963, 964, 965, 966, 967, 968, 969, 972, 973, 974, 975, 976, 977, 980, 981, 982, 983, 984, 985, 986, 987, 988, 989, 990, 991, 992, 993, 994, 995, 996, 997, 998, 999, 1000, 1005, 1006, 1007, 1008, 1009, 1014, 1015, 1016, 1017, 1018, 1019, 1020, 1021, 1022, 1025, 1026, 1027, 1028, 1029, 1030, 1031, 1033, 1034, 1035, 1036, 1037, 1038, 1039, 1043, 1044, 1045, 1046, 1047, 1048, 1049, 1051, 1052, 1053, 1055, 1056, 1057, 1058, 1059, 1060, 1061, 1062, 1063, 1066, 1067, 1068, 1069, 1070, 1071, 1072, 1073, 1080, 1081, 1082, 1083, 1084, 1085, 1088, 1089, 1090, 1091, 1094, 1095, 1096, 1097, 1098, 1099, 1100, 1101, 1102, 1103, 1104, 1105, 1106, 1107, 1108, 1109, 1110, 1111, 1113, 1114, 1115, 1116, 1117, 1118, 1119, 1120, 1121, 1122, 1123, 1124, 1125, 1126, 1127, 1128, 1129, 1130, 1135, 1136, 1137, 1138, 1139, 1140, 1141, 1142, 1143, 1144, 1146, 1147, 1148, 1149, 1153, 1154, 1155, 1156, 1157, 1158, 1159, 1160, 1161, 1162, 1163, 1164, 1165, 1166, 1167, 1168, 1169, 1172, 1173, 1174, 1175, 1176, 1177, 1178, 1179, 1180, 1181, 1182, 1183, 1187, 1188, 1189, 1190, 1191, 1192, 1193, 1196, 1199, 1200, 1201, 1203, 1204, 1205, 1206, 1207, 1209, 1210, 1211, 1212, 1213, 1214, 1215, 1216, 1217, 1218, 1222, 1223, 1224, 1225, 1226, 1227, 1228, 1229, 1230, 1231, 1234, 1235, 1236, 1237, 1238, 1239, 1240, 1242, 1243, 1244, 1245, 1246, 1247, 1248, 1249, 1250, 1251, 1255, 1256, 1257, 1258, 1259, 1260, 1261, 1262, 1263, 1264, 1265, 1266, 1267, 1268, 1269, 1270, 1271, 1277, 1278, 1280, 1281, 1282, 1283, 1284, 1285, 1286, 1293, 1294, 1295, 1296, 1297, 1298, 1299, 1300, 1302, 1303, 1304, 1305, 1306, 1307, 1310, 1311, 1312, 1313, 1314, 1316, 1318, 1319, 1320, 1321, 1322, 1323, 1324, 1325, 1326, 1327, 1328, 1329, 1330, 1335, 1336, 1337, 1338, 1339, 1340, 1341, 1342, 1343, 1344, 1345, 1346, 1347, 1348, 1349, 1351, 1353,

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2116, 2117, 2118, 2119, 2120, 2121, 2122, 2123;

(b) a nucleotide sequence encoding a polypeptide, wherein said polypeptide is selected from the
group consisting of SEQ ID NO: 2N, where N = 1- 335, SEQ ID NOs: 681, 682, 683, 690, 700,
703, 707, 715, 729, 730, 731, 743, 760, 761, 762, 763, 766, 767, 782, 783, 784, 785, 807, 808,
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1462, 1464, 1466, 1468, 1470, 1472, 1474, 1476, 1478, 1480, 1482, 1484, 1486, 1488, 1490,
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1522, 1524, 1526, 1528, 1530, 1532, 1534, 1536, 1538, 1540, 1542, 1544, 1546, 1548, 1550,
1552, 1554, and 1556;

(c) a variant of any of the nucleotide sequences of (a) or (b) that has at least 70% sequence identity
to a sequence of (a) or (b);

(d) an orthologous sequence of any of the nucleotide sequences of (a) or (b) that has at least 70%
identity to a sequence of (a) or (b);

(e) a paralogous sequence of any of the nucleotide sequences of (a) or (b) that has at least 70%
identity to a sequence of (a) or (b);

(f) a nucleotide sequence that hybridizes to any of the nucleotide sequence of (a) or (b) under
stringent conditions comprising 6x SSC and 65° C in two wash steps of 10 - 30 minutes;

(g) a nucleotide sequence encoding a polypeptide comprising a conserved domain that has at least
70% sequence homology with a conserved domain of a polypeptide encoded by any of the
nucleotide sequences of (a) – (f), wherein said conserved domain is required for the function of

the polypeptide encoded by any of the nucleotide sequences of (a) – (f) in regulating transcription and altering a trait in a transgenic plant.

2. The recombinant polynucleotide of Claim 1, wherein the recombinant polynucleotide is operably linked to at least one regulatory element being effective in controlling expression of said recombinant polynucleotide when said recombinant polynucleotide is transformed into a plant.
3. The recombinant polynucleotide of Claim 2, wherein the recombinant polynucleotide is incorporated within an expression vector.
4. The recombinant polynucleotide of Claim 3, wherein the expression vector is incorporated into a cultured host cell.
5. A transgenic plant that overexpresses the recombinant polynucleotide according to Claim 1, wherein said transgenic plant has an altered trait as compared to a non-transgenic plant or wild-type plant.
6. The transgenic plant of Claim 5, wherein said altered trait is selected from the group consisting of: increased tolerance to abiotic stress, increased tolerance to osmotic stress, increased tolerance to cold, increased germination in cold, increased tolerance to heat, increased germination in heat, increased tolerance to freezing conditions, increased tolerance to low nitrogen conditions, increased tolerance to low phosphate conditions, increased tolerance to disease, increased tolerance to fungal disease, increased tolerance to *Erysiphe*, increased tolerance to *Fusarium*, increased tolerance to *Botrytis*, increased tolerance to multiple fungal pathogens, increased resistance to glyphosate, increased sensitivity to ABA, reduced sensitivity to ABA, increased sensitivity to ACC, altered sugar sensing, increased tolerance to sugars, altered C/N sensing, early flowering, late flowering, altered flower structure, loss of flower determinacy, reduced fertility, altered shoot meristem development, altered branching pattern, altered stem morphology, altered vascular tissue structure, reduced apical dominance, altered trichome density, altered trichome development, altered trichome structure, altered root development, altered shade avoidance, altered seed development, altered seed ripening, altered seed germination, slow growth, fast growth, altered cell differentiation, altered cell proliferation, altered cell expansion, altered phase change, altered senescence, abnormal embryo development, altered programmed cell death, lethality when overexpressed, altered necrosis patterns, increased plant size, increased biomass, large seedlings, dwarfed plants, dark green leaves, change in leaf shape, increased leaf size and mass, light green or gray leaves, glossy leaves, altered abaxial/adaxial polarity, altered seed coloration, altered seed size, altered seed shape, large seed, increased leaf wax, increased leaf fatty acids, altered seed oil content, altered seed protein content, altered seed prenyl content, altered leaf prenyl lipid content, increased anthocyanin levels, and decreased anthocyanin levels.

7. The transgenic plant of Claim 5, wherein the transgenic plant is selected from the group consisting of:

soybean, potato, cotton, oilseed rape, canola, sunflower, alfalfa, clover, banana, blackberry,
 blueberry, strawberry, raspberry, cantaloupe, carrot, cauliflower, coffee, cucumber, eggplant, grapes,
 honeydew, lettuce, mango, melon, onion, papaya, peas, peppers, pineapple, pumpkin, spinach,
 squash, tobacco, tomato, tomatillo, watermelon, rosaceous fruits, fruit trees, brassicas, barley; wheat,
 corn, sweet corn, rice, rye; sugarcane, turf; millet; sorghum; currant; avocado; citrus fruits, oranges,
 lemons, grapefruit, tangerines, artichoke, cherries; walnut, peanut; endive; leek; arrowroot, beet,
 cassava, turnip, radish, yam, sweet potato; beans, pine, poplar, eucalyptus, and mint.

8. The transgenic plant of Claim 5, wherein said recombinant polynucleotide comprises a constitutive, inducible, or tissue-specific promoter operably linked to said polynucleotide sequence.

9. A method for producing a transgenic plant having an altered trait as compared to a non-transgenic or wild-type plant, the method steps comprising:

(a) providing an expression vector comprising:

(i) a recombinant polynucleotide according to Claim 1; and

(ii) at least one regulatory element flanking the polynucleotide sequence, said at least one regulatory element being effective in controlling expression of said recombinant polynucleotide in a target plant;

(b) introducing the expression vector into a plant cell, thereby producing a transgenic plant cell;

(c) growing the transgenic plant cell into a transgenic plant and allowing the transgenic plant to overexpress a polypeptide encoded by the recombinant polynucleotide, said polypeptide having the property of altering a trait in a plant as compared to a non-transgenic plant that does not overexpress the polypeptide; and

(d) identifying at least one transgenic plant with an altered trait by comparing said transgenic plant with at least one non-transgenic plant that does not overexpress the polypeptide.

10. The method of Claim 9, the method steps further comprising:

(e) selfing or crossing said at least one transgenic plant with an altered trait with itself or another plant, respectively; and

(f) growing a progeny plant from seed that develops as a result of said selfing or crossing, thus producing a transgenic progeny plant having an altered trait.

11. The method of Claim 10, wherein:

said transgenic progeny plant expresses mRNA that encodes a DNA-binding protein having a region of a conserved domain that binds to a DNA molecule, regulates expression of said DNA molecule, and induces expression of a plant trait gene; and

said mRNA is expressed at a level greater than a non-transformed plant that does not overexpress said DNA-binding protein.

12. The method of Claim 9, wherein said altered trait is increased tolerance to an osmotic stress and said osmotic stress is selected from the group consisting of drought, heat and high salt concentration.

13. The method of Claim 12, wherein said recombinant polynucleotide comprises SEQ ID NO: 2105, 2108, 2110, 2112, 2113, or 2114, or encodes a polypeptide selected from the group consisting of SEQ ID NO: 10, 12, 80, 120, 154, 156, 162, 168, 170, 172, 190, 194, 208, 216, 226, 246, 256, 264, 268, 272, 278, 288, 296, 340, 342, 346, 372, 390, 392, 404, 406, 412, 418, 426, 488, 498, 506, 530, 558, 568, 604, 612, 618, 624, 626, 656, 658, 662, 1380, 1382, and 1496.

14. The method of Claim 9, wherein said altered trait is increased tolerance to low nitrogen conditions and said recombinant polynucleotide encodes a polypeptide selected from the group consisting of SEQ ID NO: 44, 54, 116, 130, 146, 154, 166, 188, 194, 236, 244, 278, 288, 328, 380, 464, 508, 548, 590, and 610.

15. The method of Claim 9, wherein said altered trait is increased tolerance to low phosphorus conditions and said recombinant polynucleotide comprises SEQ ID NO: 2105 or encodes a polypeptide selected from the group consisting of SEQ ID NO: 80, 120, 328, 366, and 606.

16. The method of Claim 9, wherein said altered trait is increased size, growth rate or biomass and said recombinant polynucleotide comprises SEQ ID NO: 2103, 2105 or 2118, or encodes a polypeptide selected from the group consisting of SEQ ID NO: 10, 64, 70, 72, 74, 98, 120, 142, 150, 180, 188, 194, 200, 224, 228, 232, 394, 432, 468, 484, 490, 500, 502, 512, 526, 556, 608, and 632.

17. The method of Claim 9, wherein said altered trait is increased resistance or tolerance to disease and said recombinant polynucleotide encodes a polypeptide selected from the group consisting of SEQ ID NO: 278.

18. The method of Claim 17, wherein said disease is a fungal disease selected from the group consisting of *Fusarium*, *Botrytis* and *Erysiphe*-mediated diseases.

19. The method of Claim 17, wherein overexpression of said polypeptide confers resistance or tolerance to more than one pathogen.

5 20. The method of Claim 9, wherein said altered trait is a reduction or elimination of shading responses and said recombinant polynucleotide comprises SEQ ID NO: 2219 or encodes a polypeptide selected from the group consisting of SEQ ID NO: 8, 60; 408; 484; 518, 528, 578, 620, 638, 1380, and 1382.